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SEQUENCE LISTING

<110> BETTER, Marc D.
HORWITZ, Arnold H.

<120> HUMAN ENGINEERED TO ANTIBODIES TO EP-CAM

<130> 117791-072

<140> US 10/816,276
<141> 2004-03-31

<150> US 60/459,334
<151> 2003-03-31

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<170> PatentIn version 3.2

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<212> DNA
<213> Homo sapiens

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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ala	Ala	Phe	Ser	Asn	Pro	
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Val	Thr	Leu	Gly	Thr	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
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ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aag	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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cca	ggc	cag	tct	cct	cag	ctc	ctg	att	tat	cag	atg	tcc	aac	ctt	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Leu	Ala	
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tca	gga	gtc	cca	gac	agg	ttc	agt	agc	agt	ggg	tca	gga	act	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
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aca	ctg	aga	atc	agc	aga	gtg	gag	gct	gag	gat	gtg	ggt	gtt	tat	tac	336
Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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tgt	gct	caa	aat	cta	gaa	ctt	cct	cgg	acg	ttc	ggt	gga	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gly	Gly	Thr	Lys	
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Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	

NS.txt

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145	150	155	160
aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac			576
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp			
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agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa			624
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys			
185	190	195	200
gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag			672
Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln			
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 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
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 Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gly Thr Lys
 95 100 105
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<223> Mouse-Human chimeric Heavy Chain DNA and Protein Sequence

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cct gga gag aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc	144
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aca aaa tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta	192
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Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly	
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tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga	384
Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly	
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ggc tgc ctg gtc aag gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg	528
Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp	
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aac tca ggc gcc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta	576
Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu	
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Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser	
175 180 185	
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Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro	
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agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa	720
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NS.txt

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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro
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Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu
Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys
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Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
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Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
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 <223> Low Risk Human Engineered ING-1 Light Chain (LC)

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 30 35 40
 cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc 240
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288
 Ser Gly Val Pro Asp Arg Phe Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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 tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384
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 145 150 155
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 Asn Ala Leu Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
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 175 180 185
 gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
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 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60

NS.txt

Ser	Gly	Val	Pro	Asp 65	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp 75	Phe
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Cys	Ala	Gln 95	Asn	Leu	Glu	Leu	Pro 100	Arg	Thr	Phe	Gly	Gln 105	Gly	Thr	Lys
Leu	Glu 110	Met	Lys	Arg	Thr	Val 115	Ala	Ala	Pro	Ser	Val 120	Phe	Ile	Phe	Pro
Pro 125	Ser	Asp	Glu	Gln	Leu 130	Lys	Ser	Gly	Thr	Ala 135	Ser	Val	Val	Cys	Leu 140
Leu	Asn	Asn	Phe	Tyr 145	Pro	Arg	Glu	Ala	Lys 150	Val	Gln	Trp	Lys	Val 155	Asp
Asn	Ala	Leu	Gln 160	Ser	Gly	Asn	Ser	Gln 165	Glu	Ser	Val	Thr	Glu 170	Gln	Asp
Ser	Lys	Asp 175	Ser	Thr	Tyr	Ser	Leu 180	Ser	Ser	Thr	Leu	Thr 185	Leu	Ser	Lys
Ala	Asp 190	Tyr	Glu	Lys	His	Lys 195	Val	Tyr	Ala	Cys	Glu 200	Val	Thr	His	Gln
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Gly	Ser	Thr	Ala -1	Asp 1	Ile	Val	Met	Thr 5	Gln	Ser	Pro	Leu	Ser	Leu	Pro	
gtc	act	cct	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
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Ser	Gly	Val	Pro	Asp 65	Arg	Phe	Ser	Ser 70	Ser	Gly	Ser	Gly	Thr	Asp 75	Phe	
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Thr	Leu	Lys 80	Ile	Ser	Arg	Val	Glu 85	Ala	Glu	Asp	Val	Gly 90	Val	Tyr	Tyr	
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Cys	Ala	Gln 95	Asn	Leu	Glu	Leu	Pro 100	Arg	Thr	Phe	Gly	Gln 105	Gly	Thr	Lys	

NS.txt																		
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp			
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agc	aag	gac	agc	acc	tac	agc	ctc	agc	acc	ctg	acg	ctg	agc	aaa			624	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys			
			175				180					185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag		672	
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln			
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ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag		720	
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205					210					215								

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Pro	Gly	Gln	Ser	Pro	Gln	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala			
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Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe		
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Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys		
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			160					165					170				
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys		
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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln		
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205					210					215							

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 <223> KL1 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

 <400> 9
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 atccactgca gacatcgtga tgacccag 88

 <210> 10
 <211> 85
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> KL2 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

 <400> 10
 actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag 60
 tgcagactgg gtcatcacga tgtct 85

 <210> 11
 <211> 88
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> KL3 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 gcagaaacca gggcagtctc ctcagctg 88

 <210> 12
 <211> 86
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <223> KL4 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

 <400> 12
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 <210> 13
 <211> 77
 <212> DNA
 <213> Homo sapiens

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 <223> KL5 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 ggagtttatt actgtgc 77

 <210> 14
 <211> 75

<212> DNA
 <213> Homo sapiens

 <220>
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 <223> KL6 V Region Oligos Human Engineered ING-1 Light Chain (Kappa low)

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 gtaataaact cccac 75

 <210> 15
 <211> 22
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> Low Risk Primers Forward Primer: KF ING-1 Light Chain Oligos

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 <210> 16
 <211> 21
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 <223> Low risk Primers Reverse Primer: KR ING-1 Light Chain Oligos

 <400> 16
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 <210> 17
 <211> 85
 <212> DNA
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 <223> Moderate Risk Primer: KM2 V Region Oligos Human Engineered ING-1
 Light Chain Oligos (Kappa Moderate)

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 <210> 18
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 <223> Low Risk Human Engineered ING-1 Heavy Chain (HC)

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 <223> Variable region of HC is Amino Acids is 1-116

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<221> CDS
 <222> (1)..(1395)

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 gcc caa gca cag atc cag ttg gtg cag tct gga cct gag gtg aag aag 96
 Ala Gln Ala Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Val Lys Lys
 -1 1 5 10
 cct gga gag tcc gtc aag atc tcc tgc aag gct tct gga tat acc ttc 144
 Pro Gly Glu Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 15 20 25
 aca aaa tat gga atg aac tgg gtg aag cag gct cca gga cag ggt tta 192
 Thr Lys Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Gln Gly Leu
 30 35 40 45
 aag tgg atg ggc tgg ata aac acc tac act gaa gag cca aca tat ggt 240
 Lys Trp Met Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly
 50 55 60
 gat gac ttc aag gga cgg ttt acc ttc acc ttg gac acc tct act agc 288
 Asp Asp Phe Lys Gly Arg Phe Thr Phe Thr Leu Asp Thr Ser Thr Ser
 65 70 75
 act gcc tat ttg gaa atc tct tct ctc cgg agt gag gac acg gct aca 336
 Thr Ala Tyr Leu Glu Ile Ser Ser Leu Arg Ser Glu Asp Thr Ala Thr
 80 85 90
 tat ttc tgt gca aga ttt ggc tct gct gtg gac tac tgg ggt caa gga 384
 Tyr Phe Cys Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly
 95 100 105
 acc ttg gtc acc gtc tcc tca gcc agc aca aag ggc cca tcg gtc ttc 432
 Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
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 ccc ctg gca ccc tcc aag agc acc tct ggg ggc aca gcg gcc ctg 480
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140
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 Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155
 aac tca ggc ggc ctg acc agc ggc gtg cac acc ttc ccg gct gtc cta 576
 Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 160 165 170
 cag tcc tca gga ctc tac tcc ctc agc agc gtg gtg acc gtg ccc tcc 624
 Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 175 180 185
 agc agc ttg ggc acc cag acc tac atc tgc aac gtg aat cac aag ccc 672
 Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 190 195 200 205
 agc aac acc aag gtg gac aag aga gtt gag ccc aaa tct tgt gac aaa 720
 Ser Asn Thr Lys Val Asp Lys Arg Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220 225
 act cac aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg 768
 Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 230 235
 tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc 816
 Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 240 245 250
 cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac 864
 Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 255 260 265
 cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat 912

NS.txt																
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Val	Ser	Val	Thr 305	Val	Val	Leu	His	Asp 310	Trp	Leu	Asn	Gly 315	Lys	Glu		
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Tyr	Lys	Cys 320	Lys	Val	Ser	Asn	Lys 325	Ala	Leu	Pro	Ala	Pro 330	Ile	Glu	Lys	
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Thr	Ile 335	Ser	Lys	Ala	Lys	Gly 340	Gln	Pro	Arg	Glu	Pro 345	Gln	Val	Tyr	Thr	
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Leu	Pro	Pro	Ser	Arg	Asp 355	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr 365	
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Ser	Asn	Gly 385	Gln	Pro	Glu	Asn	Asn	Tyr 390	Lys	Thr	Thr	Pro 395	Pro	Val	Leu	
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296
Asp	Ser	Asp 400	Gly	Ser	Phe	Phe	Leu 405	Tyr	Ser	Lys	Leu	Thr 410	Val	Asp	Lys	
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Lys																

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 <212> PRT
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Pro	Gly -1	Glu	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Lys	Gln	Ala	Pro	Gly	Gln	Gly	Leu
Lys	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly
Asp	Asp	Phe	Lys	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser
Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Thr
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe
Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu
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NS.txt																
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Thr	Lys	Tyr	Gly	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
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Glu	Trp	Met	Gly	Trp	Ile	Asn	Thr	Tyr	Thr	Glu	Glu	Pro	Thr	Tyr	Gly	
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cag	aag	ttc	cag	gga	cgg	ttt	acc	ttc	acc	ttg	gac	acc	tct	act	agc	288
Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	
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Thr	Ala	Tyr	Leu	Glu	Ile	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
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tat	ttc	tgt	gca	aga	ttt	ggc	tct	gct	gtg	gac	tac	tgg	ggt	caa	gga	384
Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
	95					100				105						
acc	ttg	gtc	acc	gtc	tcc	tca	gcc	agc	aca	aag	ggc	cca	tcg	gtc	ttc	432
Thr	Leu	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	
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Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	
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ggc	tgc	ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	528
Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	
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Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
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cag	tcc	tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	624
Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
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agc	agc	ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	672
Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	
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Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
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Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
			225					230					235			
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Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
		240					245					250				
cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	cac	gaa	gac	864
Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
		255				260				265						
cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	gtg	cat	aat	912
Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	
					275					280					285	
gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	acg	tac	cgg	gtg	960
Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	
				290					295					300		
gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	aat	ggc	aag	gag	1008
Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	
			305					310					315			
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Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	
		320					325					330				
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Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp 375	Ile	Ala	Val	Glu	Trp	Glu	
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Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	
gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tac	agc	aag	ctc	acc	gtg	gac	aag	1296
Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	
agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	gtg	atg	cat	gag	1344
Ser	Arg	Trp	Gln	Gln	Gly	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu		
gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	ctg	tct	ccg	ggc	1392
Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
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Lys																

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Gln	Lys	Phe	Gln	Gly	Arg	Phe	Thr	Phe	Thr	Leu	Asp	Thr	Ser	Thr	Ser	
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Tyr	Phe	Cys	Ala	Arg	Phe	Gly	Ser	Ala	Val	Asp	Tyr	Trp	Gly	Gln	Gly	
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Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	
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Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
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	190				195					200					205	
Ser	Asn	Thr	Lys	Val	Asp	Lys	Arg	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	
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Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Pro	
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Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile	Ser	
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Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu	Asp	
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Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His	Asn	

NS.txt

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	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr
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	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr
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	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
				370						375					380	
	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu
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	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys
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	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu
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 (gamma low)

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 <223> GL2 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 23
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 cttcacctca ggtccagact gcaccaactg 90

<210> 24
 <211> 91
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL3 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 24
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NS.txt 91

aaagtggatg ggctggataa acacctacac t

<210> 25
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL4 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 25
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 ttggctcttc agtgtagggtg tttatccagc 90

<210> 26
 <211> 90
 <212> DNA
 <213> Homo sapiens

<220>
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 <223> GL5 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

<400> 26
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 acatatttct gtgcaagatt tggctctgct 90

<210> 27
 <211> 85
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> GL6 V Region Oligos: Human Engineered ING-1 Heavy Chain Oligos
 (gamma low)

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 gtccacagca gagccaaatc ttgca 85

<210> 28
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 <212> DNA
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 <223> Human Engineered ING-1 Heavy Chain Oligos-Low Risk Primers
 Forward primer:GF

<400> 28
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<210> 29
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 <223> Human Engineered ING-1 Heavy Chain Oligos Low Risk Primers
 -Reverse Primer GR

 <220>
 <221> misc_feature
 <223> ING-1 Heavy Chain Oligos Low Risk Primers Reverse Primer GR

 <400> 29
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 <210> 30
 <211> 90
 <212> DNA
 <213> Homo sapiens

 <220>
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 <223> GM2 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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 <213> Homo sapiens

 <220>
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 <223> GM3 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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 <220>
 <221> misc_feature
 <223> GM4 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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 <223> GM5 V Region Oligos Human Engineered ING-1 Heavy Chain Oligos-Low
 + Moderate Risk Primers

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<400> 33
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<210> 34
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<212> DNA
<213> Homo sapiens

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<223> P1=P Human Engineered (low risk) ING1 light Chain with one
      moderate risk proline change; proline at position 8 (P1)

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<222> (1)..(717)

<220>
<221> mat_peptide
<222> (61)..()

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      -20 -15 -10 -5
      gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca 96
      Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
      -1 1 5 10
      gtc act ctg gga gag tca ggt tcc atc tcc tgc cgg tct agt aag agt 144
      Val Thr Leu Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
      15 20 25
      ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192
      Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
      30 35 40
      cca ggg cag tct cct cag ctg ctc atc tat cag atg tct aac aga gcc 240
      Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
      45 50 55 60
      tca ggg gtc cca gac agg ttc agt agc agt gga tct ggg aca gat ttc 288
      Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
      65 70 75
      act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336
      Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
      80 85 90
      tgt gct cag aac cta gag ctt ccg cgg acg ttc ggt cag ggc acc aag 384
      Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
      95 100 105
      ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 432
      Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
      110 115 120
      cca tct gat gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg 480
      Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
      125 130 135 140
      ctg aat aac ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat 528
      Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
      145 150 155
      aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
      Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
      160 165 170
      agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
      Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
      175 180 185
      gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672

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Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
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<213> Homo sapiens
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		Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys
		Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
		Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe
		Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
		Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
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		Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
		Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
		Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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<211> 720
<212> DNA
<213> Homo sapiens
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<220>
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<223> P2=P Human Engineered (low risk) ING1 light Chain with one
moderate risk proline change; proline at position 15 (P2)
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<220>
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<222> (61)..()
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Page 20

NS.txt

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Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
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gtc	act	cct	gga	gag	tca	ggg	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
Val	Thr	Pro	Gly	Glu	Ser	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
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ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
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Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45					50					55					60	
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65				70						75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
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tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
		95					100					105				
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
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Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
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Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
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gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
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 <211> 239
 <212> PRT
 <213> Homo sapiens

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 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75

NS.txt																
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Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
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ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
				145					150					155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
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agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
			175				180					185				
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
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ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
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<210> 39
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 <212> PRT
 <213> Homo sapiens

<400> 39

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		15					20					25			
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys
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Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala
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Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr
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Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys
		95					100					105			
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro
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Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu
					130					135					140
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp
				145					150					155	
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			160					165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
			175				180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
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<210> 40
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 <212> DNA
 <213> Homo sapiens

<220>
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 <223> P1P2=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 15(P2)

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<220>
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 gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca 96
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
 -1 1 5 10
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 Val Thr Pro Gly Glu Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25
 ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa 192
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 cca ggg cag tct cct cag ctg ctg atc tat cag atg tct aac aga gcc 240
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
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 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 act ctc aag atc agc aga gtg gag gct gaa gat gtg gga gtt tat tac 336
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
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 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 ctt gag atg aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg 432
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 110 115 120
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 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
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 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
 aac gcc ctc caa tcg ggt aac tcc cag gag agt gtc aca gag cag gac 576
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 agc aag gac agc acc tac agc ctc agc agc acc ctg acg ctg agc aaa 624
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 gca gac tac gag aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag 672
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
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 ggc ctg agc tcg ccc gtc aca aag agc ttc aac agg gga gag tgt tag 720
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 205 210 215

<210> 41
 <211> 239
 <212> PRT

<213> Homo. sapiens

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-1  1  5  10
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30 35 40
Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
45 50 55 60
Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
65 70 75
Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
80 85 90
Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
95 100 105
Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
110 115 120
Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
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145 150 155
Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
160 165 170
Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
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Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
205 210 215

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<210> 42

<211> 720

<212> DNA

<213> Homo sapiens

<220>

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<223> P1P3= Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

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<220>

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<222> (61)..()

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<400> 42
atg agg ttc tct gct cag ctt ctg ggg ctg ctt gtg ctc tgg atc cct      48
Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
-20      -15      -10      -5
gga tcc act gca gac atc gtg atg acc cag tct cca ctc tcc aat cca      96
Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
-1  1  5  10
gtc act ctg gga gag ccg ggt tcc atc tcc tgc cgg tct agt aag agt      144
Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
15 20 25
ctc cta cat agt aat ggc atc act tat ttg tat tgg tat ctg cag aaa      192

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NS.txt																
Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
30	30					35				40						
cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
45					50					55					60	
tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
				65					70					75		
act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
			80					85					90			
tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggg	cag	ggc	acc	aag	384
Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
		95					100					105				
ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
	110					115					120					
cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
125					130					135					140	
ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
				145				150						155		
aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
			160					165					170			
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa	624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	
		175					180				185					
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag	672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	
	190					195					200					
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag	720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys		
205					210					215						

<210> 43
 <211> 239
 <212> PRT
 <213> Homo sapiens

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 Met Arg Phe Ser Ala Gln Leu Leu Gly Leu Leu Val Leu Trp Ile Pro
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 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Pro Leu Ser Asn Pro
 -1 1
 Val Thr Leu Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Lys Ser
 15 20 25
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp

NS.txt

Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp
			160					165					170		
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys
		175					180					185			
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln
	190					195					200				
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys	
205					210					215					

<210> 44
 <211> 720
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> P2P3=Human Engineered (low risk) ING1 light Chain with one moderate risk proline change; proline at position 8 (P1) 18 (P3)

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <221> mat_peptide
 <222> (61)..()

<400> 44	atg	agg	ttc	tct	gct	cag	ctt	ctg	ggg	ctg	ctt	gtg	ctc	tgg	atc	cct	48
	Met	Arg	Phe	Ser	Ala	Gln	Leu	Leu	Gly	Leu	Leu	Val	Leu	Trp	Ile	Pro	
	-20					-15					-10					-5	
	gga	tcc	act	gca	gac	atc	gtg	atg	acc	cag	tct	gca	ctc	tcc	aat	cca	96
	Gly	Ser	Thr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	Ala	Leu	Ser	Asn	Pro	
				-1	1			5					10				
	gtc	act	cct	gga	gag	ccg	ggt	tcc	atc	tcc	tgc	cgg	tct	agt	aag	agt	144
	Val	Thr	Pro	Gly	Glu	Pro	Gly	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Lys	Ser	
			15				20					25					
	ctc	cta	cat	agt	aat	ggc	atc	act	tat	ttg	tat	tgg	tat	ctg	cag	aaa	192
	Leu	Leu	His	Ser	Asn	Gly	Ile	Thr	Tyr	Leu	Tyr	Trp	Tyr	Leu	Gln	Lys	
			30			35					40						
	cca	ggg	cag	tct	cct	cag	ctg	ctc	atc	tat	cag	atg	tct	aac	aga	gcc	240
	Pro	Gly	Gln	Ser	Pro	Gln	Leu	Leu	Ile	Tyr	Gln	Met	Ser	Asn	Arg	Ala	
	45					50					55					60	
	tca	ggg	gtc	cca	gac	agg	ttc	agt	agc	agt	gga	tct	ggg	aca	gat	ttc	288
	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Ser	Ser	Gly	Ser	Gly	Thr	Asp	Phe	
					65				70						75		
	act	ctc	aag	atc	agc	aga	gtg	gag	gct	gaa	gat	gtg	gga	gtt	tat	tac	336
	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	
				80					85					90			
	tgt	gct	cag	aac	cta	gag	ctt	ccg	cgg	acg	ttc	ggt	cag	ggc	acc	aag	384
	Cys	Ala	Gln	Asn	Leu	Glu	Leu	Pro	Arg	Thr	Phe	Gly	Gln	Gly	Thr	Lys	
			95					100				105					
	ctt	gag	atg	aaa	cga	act	gtg	gct	gca	cca	tct	gtc	ttc	atc	ttc	ccg	432
	Leu	Glu	Met	Lys	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	
			110				115					120					
	cca	tct	gat	gag	cag	ttg	aaa	tct	gga	act	gcc	tct	gtt	gtg	tgc	ctg	480
	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	
						130					135					140	
	ctg	aat	aac	ttc	tat	ccc	aga	gag	gcc	aaa	gta	cag	tgg	aag	gtg	gat	528
	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	
					145					150					155		
	aac	gcc	ctc	caa	tcg	ggt	aac	tcc	cag	gag	agt	gtc	aca	gag	cag	gac	576

									NS.txt									
Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp			
			160					165					170					
agc	aag	gac	agc	acc	tac	agc	ctc	agc	agc	acc	ctg	acg	ctg	agc	aaa			624
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys			
		175					180					185						
gca	gac	tac	gag	aaa	cac	aaa	gtc	tac	gcc	tgc	gaa	gtc	acc	cat	cag			672
Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln			
	190					195					200							
ggc	ctg	agc	tcg	ccc	gtc	aca	aag	agc	ttc	aac	agg	gga	gag	tgt	tag			720
Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
205					210					215								

<210> 45
 <211> 239
 <212> PRT
 <213> Homo sapiens

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 -20 -15 -10 -5
 Gly Ser Thr Ala Asp Ile Val Met Thr Gln Ser Ala Leu Ser Asn Pro
 -1 1 5 10
 Val Thr Pro Gly Glu Pro Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser
 15 20 25
 Leu Leu His Ser Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys
 30 35 40
 Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Arg Ala
 45 50 55 60
 Ser Gly Val Pro Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe
 65 70 75
 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
 80 85 90
 Cys Ala Gln Asn Leu Glu Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys
 95 100 105
 Leu Glu Met Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro
 110 115 120
 Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu
 125 130 135 140
 Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp
 145 150 155
 Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp
 160 165 170
 Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 175 180 185
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln
 190 195 200
 Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 205 210 215

<210> 46
 <211> 85
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> P1 Oligo Human Engineered ING-1 with proline oligos

<400> 46
 actcttacta gaccggcagg agatggaacc tgactctccc agagtgactg gattggagag
 tggagactgg gtcatcacga tgtct 60
 85

<210> 47

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<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P2 Oligo Human Engineered ING-1 with proline oligos

<400> 47
      actcttacta gaccggcagg agatggaacc tgactctcca ggagtgactg gattggagag      60
      tgcagactgg gtcatcacga tgtct                                           85

<210> 48
<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P3 Oligo Human Engineered ING-1 with proline oligos

<400> 48
      actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag      60
      tgcagactgg gtcatcacga tgtct                                           85

<210> 49
<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P1P2 Oligo Human Engineered ING-1 with proline oligos

<400> 49
      actcttacta gaccggcagg agatggaacc cggctctcca ggagtgactg gattggagag      60
      tgcagactgg gtcatcacga tgtct                                           85

<210> 50
<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P1P3 Oligo Human Engineered ING-1 with proline oligos

<400> 50
      actcttacta gaccggcagg agatggaacc cggctctccc agagtgactg gattggagag      60
      tggagactgg gtcatcacga tgtct                                           85

<210> 51
<211> 85
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> P2P3 Oligo Human Engineered ING-1 with proline oligos

<400> 51
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      tgcagactgg gtcatcacga tgtct                                           85

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<210> 52
 <211> 19
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Reverse Primer KBsr ING-1 Light Chain

<400> 52
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19

<210> 53
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> EpCam truncated sequence

<220>
 <221> CDS
 <222> (1)..(795)

<400> 53
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 Met Ala Pro Pro Gln Val Leu Ala Phe Gly Leu Leu Leu Ala Ala Ala
 1 5 10 15
 acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac 96
 Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
 20 25 30
 aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt 144
 Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
 35 40 45
 act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc 192
 Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
 50 55 60
 aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga 240
 Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
 65 70 75 80
 aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat 288
 Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
 85 90 95
 cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc 336
 Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
 100 105 110
 acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac 384
 Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
 115 120 125
 aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc 432
 Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
 130 135 140
 atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa 480
 Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
 145 150 155 160
 agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg 528
 Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
 165 170 175
 gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act 576
 Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
 180 185 190

									NS.txt										
att	gat	ctg	gtt	caa	aat	tct	tct	caa	aaa	act	cag	aat	gat	gtg	gac				624
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp				
		195					200					205							
ata	gct	gat	gtg	gct	tat	tat	ttt	gaa	aaa	gat	gtt	aaa	ggg	gaa	tcc				672
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser				
	210					215					220								
ttg	ttt	cat	tct	aag	aaa	atg	gac	ctg	aca	gta	aat	ggg	gaa	caa	ctg				720
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu				
	225				230					235					240				
gat	ctg	gat	cct	ggg	caa	act	tta	att	tat	tat	gtt	gat	gaa	aaa	gca				768
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala				
				245					250					255					
cct	gaa	ttc	tca	atg	cag	ggg	cta	aaa	taa										798
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys											
			260					265											

<210> 54
 <211> 265
 <212> PRT
 <213> Homo sapiens

<400> 54

Met	Ala	Pro	Pro	Gln	Val	Leu	Ala	Phe	Gly	Leu	Leu	Leu	Ala	Ala	Ala
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Thr	Ala	Thr	Phe	Ala	Ala	Ala	Gln	Glu	Glu	Cys	Val	Cys	Glu	Asn	Tyr
			20					25					30		
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys
		35				40						45			
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala
	50					55					60				
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg
65				70						75					80
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp
			85						90					95	
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly
			100					105					110		
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp
		115					120					125			
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile
	130					135					140				
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys
145					150					155					160
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu
				165					170					175	
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr
			180					185					190		
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp
		195					200					205			
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser
	210					215					220				
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu
225					230					235					240
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala
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Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys							
			260					265							

<210> 55
 <211> 945
 <212> DNA
 <213> Homo sapiens

<220>

<221> misc_feature

<223> Full-Length EpCam

<220>

<221> CDS

<222> (1)..(942)

<220>

<221> mat_peptide

<222> (70)..()

<400>

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-20 -15 -10
acg gcg act ttt gcc gca gct cag gaa gaa tgt gtc tgt gaa aac tac      96
Thr Ala Thr Phe Ala Ala Ala Gln Glu Glu Cys Val Cys Glu Asn Tyr
-5 -1 1 5
aag ctg gcc gta aac tgc ttt gtg aat aat aat cgt caa tgc cag tgt      144
Lys Leu Ala Val Asn Cys Phe Val Asn Asn Asn Arg Gln Cys Gln Cys
10 15 20 25
act tca gtt ggt gca caa aat act gtc att tgc tca aag ctg gct gcc      192
Thr Ser Val Gly Ala Gln Asn Thr Val Ile Cys Ser Lys Leu Ala Ala
30 35 40
aaa tgt ttg gtg atg aag gca gaa atg aat ggc tca aaa ctt ggg aga      240
Lys Cys Leu Val Met Lys Ala Glu Met Asn Gly Ser Lys Leu Gly Arg
45 50 55
aga gca aaa cct gaa ggg gcc ctc cag aac aat gat ggg ctt tat gat      288
Arg Ala Lys Pro Glu Gly Ala Leu Gln Asn Asn Asp Gly Leu Tyr Asp
60 65 70
cct gac tgc gat gag agc ggg ctc ttt aag gcc aag cag tgc aac ggc      336
Pro Asp Cys Asp Glu Ser Gly Leu Phe Lys Ala Lys Gln Cys Asn Gly
75 80 85
acc tcc acg tgc tgg tgt gtg aac act gct ggg gtc aga aga aca gac      384
Thr Ser Thr Cys Trp Cys Val Asn Thr Ala Gly Val Arg Arg Thr Asp
90 95 100 105
aag gac act gaa ata acc tgc tct gag cga gtg aga acc tac tgg atc      432
Lys Asp Thr Glu Ile Thr Cys Ser Glu Arg Val Arg Thr Tyr Trp Ile
110 115 120
atc att gaa cta aaa cac aaa gca aga gaa aaa cct tat gat agt aaa      480
Ile Ile Glu Leu Lys His Lys Ala Arg Glu Lys Pro Tyr Asp Ser Lys
125 130 135
agt ttg cgg act gca ctt cag aag gag atc aca acg cgt tat caa ctg      528
Ser Leu Arg Thr Ala Leu Gln Lys Glu Ile Thr Thr Arg Tyr Gln Leu
140 145 150
gat cca aaa ttt atc acg agt att ttg tat gag aat aat gtt atc act      576
Asp Pro Lys Phe Ile Thr Ser Ile Leu Tyr Glu Asn Asn Val Ile Thr
155 160 165
att gat ctg gtt caa aat tct tct caa aaa act cag aat gat gtg gac      624
Ile Asp Leu Val Gln Asn Ser Ser Gln Lys Thr Gln Asn Asp Val Asp
170 175 180 185
ata gct gat gtg gct tat tat ttt gaa aaa gat gtt aaa ggt gaa tcc      672
Ile Ala Asp Val Ala Tyr Tyr Phe Glu Lys Asp Val Lys Gly Glu Ser
190 195 200
ttg ttt cat tct aag aaa atg gac ctg aca gta aat ggg gaa caa ctg      720
Leu Phe His Ser Lys Lys Met Asp Leu Thr Val Asn Gly Glu Gln Leu
205 210 215
gat ctg gat cct ggt caa act tta att tat tat gtt gat gaa aaa gca      768
Asp Leu Asp Pro Gly Gln Thr Leu Ile Tyr Tyr Val Asp Glu Lys Ala
220 225 230
cct gaa ttc tca atg cag ggt cta aaa gct ggt gtt att gct gtt att      816
Pro Glu Phe Ser Met Gln Gly Leu Lys Ala Gly Val Ile Ala Val Ile
235 240 245

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gtg	gtt	gtg	gtg	ata	gca	gtt	gtt	gct	gga	att	gtt	gtg	ctg	gtt	att	864
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile	
250					255					260					265	
tcc	aga	aag	aag	aga	atg	gca	aag	tat	gag	aag	gct	gag	ata	aag	gag	912
Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu	
				270					275					280		
atg	ggt	gag	atg	cat	agg	gaa	ctc	aat	gca	taa						945
Met	Gly	Glu	Met	His	Arg	Glu	Leu	Asn	Ala							
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 <213> Homo sapiens

<400> 56

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		-5				-1	1				5					
Lys	Leu	Ala	Val	Asn	Cys	Phe	Val	Asn	Asn	Asn	Arg	Gln	Cys	Gln	Cys	
10				15				20						25		
Thr	Ser	Val	Gly	Ala	Gln	Asn	Thr	Val	Ile	Cys	Ser	Lys	Leu	Ala	Ala	
			30					35					40			
Lys	Cys	Leu	Val	Met	Lys	Ala	Glu	Met	Asn	Gly	Ser	Lys	Leu	Gly	Arg	
		45						50					55			
Arg	Ala	Lys	Pro	Glu	Gly	Ala	Leu	Gln	Asn	Asn	Asp	Gly	Leu	Tyr	Asp	
		60					65				70					
Pro	Asp	Cys	Asp	Glu	Ser	Gly	Leu	Phe	Lys	Ala	Lys	Gln	Cys	Asn	Gly	
	75					80					85					
Thr	Ser	Thr	Cys	Trp	Cys	Val	Asn	Thr	Ala	Gly	Val	Arg	Arg	Thr	Asp	
90				95						100					105	
Lys	Asp	Thr	Glu	Ile	Thr	Cys	Ser	Glu	Arg	Val	Arg	Thr	Tyr	Trp	Ile	
			110					115						120		
Ile	Ile	Glu	Leu	Lys	His	Lys	Ala	Arg	Glu	Lys	Pro	Tyr	Asp	Ser	Lys	
			125					130					135			
Ser	Leu	Arg	Thr	Ala	Leu	Gln	Lys	Glu	Ile	Thr	Thr	Arg	Tyr	Gln	Leu	
		140					145					150				
Asp	Pro	Lys	Phe	Ile	Thr	Ser	Ile	Leu	Tyr	Glu	Asn	Asn	Val	Ile	Thr	
	155					160					165					
Ile	Asp	Leu	Val	Gln	Asn	Ser	Ser	Gln	Lys	Thr	Gln	Asn	Asp	Val	Asp	
170				175						180					185	
Ile	Ala	Asp	Val	Ala	Tyr	Tyr	Phe	Glu	Lys	Asp	Val	Lys	Gly	Glu	Ser	
			190					195						200		
Leu	Phe	His	Ser	Lys	Lys	Met	Asp	Leu	Thr	Val	Asn	Gly	Glu	Gln	Leu	
			205					210					215			
Asp	Leu	Asp	Pro	Gly	Gln	Thr	Leu	Ile	Tyr	Tyr	Val	Asp	Glu	Lys	Ala	
		220					225					230				
Pro	Glu	Phe	Ser	Met	Gln	Gly	Leu	Lys	Ala	Gly	Val	Ile	Ala	Val	Ile	
	235					240					245					
Val	Val	Val	Val	Ile	Ala	Val	Val	Ala	Gly	Ile	Val	Val	Leu	Val	Ile	
250				255						260					265	
Ser	Arg	Lys	Lys	Arg	Met	Ala	Lys	Tyr	Glu	Lys	Ala	Glu	Ile	Lys	Glu	
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<221> misc_feature
<223> Forward Primer (for both soluble and full length Ep-CAM): EC-1

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<211> 31
<212> DNA
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<220>
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<223> Ep-CAM Reverse Primer (for soluble Ep-CAM): EC-2

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31

<210> 59
<211> 30
<212> DNA
<213> Homo sapiens

<220>
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<223> Ep-CAM Reverse Primer (for full-length Ep-CAM): EC-3

<400> 59
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<220>
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<223> Variable Region for Mouse-Human Chimeric ING-1 Light Chain

<400> 60

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1           5           10           15

Thr Ser Gly Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu His Ser
20           25           30

Asn Gly Ile Thr Tyr Leu Tyr Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35           40           45

Pro Gln Leu Leu Ile Tyr Gln Met Ser Asn Leu Ala Ser Gly Val Pro
50           55           60

Asp Arg Phe Ser Ser Ser Gly Ser Gly Thr Asp Phe Thr Leu Arg Ile
65           70           75           80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Ala Gln Asn

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85

90

95

Leu Glu Leu Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Met Lys
 100 105 110

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 <211> 116
 <212> PRT
 <213> Homo sapiens

<220>
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 <223> Variable Region for Mouse-Human Chimeric ING-1 Heavy Chain
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Gln Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu
 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Lys Tyr
 20 25 30

Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met
 35 40 45

Gly Trp Ile Asn Thr Tyr Thr Glu Glu Pro Thr Tyr Gly Asp Asp Phe
 50 55 60

Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr Ala Asn
 65 70 75 80

Leu Gln Ile Asn Asn Leu Lys Ser Glu Asp Thr Ala Thr Tyr Phe Cys
 85 90 95

Ala Arg Phe Gly Ser Ala Val Asp Tyr Trp Gly Gln Gly Thr Ser Val
 100 105 110

Thr Val Ser Ser
 115